

Amendments to the Specification:

I. Please replace the paragraph on page 16, lines 16-21 with the following amended paragraph:

The term "nucleotide sequence complementary to the nucleotide sequence of Table 1" refers to the nucleotide sequence of the complementary strand of a ~~nucleic acid strand~~ nucleotide sequence having a SEQ ID NO: designated in ~~the GenBank accession referred to in~~ Table 1. The term "complementary strand" is used herein interchangeably with the term "complement". The complement of a nucleic acid strand can be the complement of a coding strand or the complement of a non-coding strand.

II. Please replace the paragraph on page 17, lines 15-24 with the following amended paragraph:

As used herein, the term "specifically hybridizes" or "specifically detects" refers to the ability of a nucleic acid molecule of the invention to hybridize to at least a portion of, for example, approximately 6, 12, 15, 20, 30, 50, 100, 150, 200, 300, 350, 400, 500, 750, or 1000 contiguous nucleotides of a nucleic acid designated in any one of ~~SEQ ID Nos: 1-146~~ SEQ ID NOS:1-145, or a sequence complementary thereto, or naturally occurring mutants thereof, such that it has less than 15%, preferably less than 10%, and more preferably less than 5% background hybridization to a cellular nucleic acid (e.g., mRNA or genomic DNA) encoding a different protein. In preferred embodiments, the oligonucleotide probe detects only a specific nucleic acid, e.g., it does not substantially hybridize to similar or related nucleic acids, or complements thereof.

III. Please replace the paragraph on page 46, line 25 to page 47, line 5 with the following amended paragraph:

In yet another embodiment, the invention provides methods for determining whether a subject is at risk for developing a disease, such as a predisposition to develop IBD, for example UC or CD, associated with an aberrant activity of any one of the polypeptides encoded by

nucleic acids of ~~SEQ ID Nos: 1-146~~ SEQ ID NOS:1-145, wherein the aberrant activity of the polypeptide is characterized by detecting the presence or absence of a genetic lesion characterized by at least one of (i) an alteration affecting the integrity of a gene encoding a marker polypeptides, or (ii) the mis-expression of the encoding nucleic acid. To illustrate, such genetic lesions can be detected by ascertaining the existence of at least one of (i) a deletion of one or more nucleotides from the nucleic acid sequence, (ii) an addition of one or more nucleotides to the nucleic acid sequence, (iii) a substitution of one or more nucleotides of the nucleic acid sequence, (iv) a gross chromosomal rearrangement of the nucleic acid sequence, (v) a gross alteration in the level of a messenger RNA transcript of the nucleic acid sequence, (vi) aberrant modification of the nucleic acid sequence, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild type splicing pattern of a messenger RNA transcript of the gene, (viii) a non-wild type level of the marker polypeptide, (ix) allelic loss of the gene, and/or (x) inappropriate post-translational modification of the marker polypeptide.

IV. Please replace Table 1 on pages 51-59 with the following amended Table 1:

Table 1.

	UC	CD	Accession No. SEQ ID NO:	Gene Names	Chromosome	Microsatellite Markers
I	121.4	112.8	Y000787 <u>1</u>	MDNCF/IL-8	4q13-q21	D4S392-D4S2947
I	115.3		X54489 <u>2</u>	MGSA (GRO1)	4q21	D4S400-D4S1534
I	17.9		M57731 <u>3</u>	MIP-2 α (GRO2)	4q21	D4S392-D4S2947
I	18.9	14.1	M28130 <u>4</u>	IL8	4q13-q21	D4S392-D4S2947
I	16.8	13.9	X57351 <u>5</u>	IP-10 IFITM2	11	pTEL-D11S1318
I	16		J04130 <u>6</u>	MIP-1 β /SCYA4	17q21	D17S933-D17S800
I	13.4		X53800 <u>7</u>	MIP-2 β (GRO3)	4q21	D4S400-D4S1534
I	13.2		M69203 <u>8</u>	MIP-1β/SCYA2 MIP-1β/SCYA4	17q21	D17S933-D17S800
I	14.6		X04500 <u>9</u>	pro-IL-1 β	2q14	D2S293-D2S121
I	13.5		X53296 <u>10</u>	IL-1RA	2q14	D2S293-D2S121
I	13.3		X04602 <u>11</u>	IL-6	7q21	D7S829-D7S673
I	13		J03756 <u>12</u>	Growth hormone 2 (GH2)	17q22-q24	D17S794-D17S795
I	13.5		D16431 <u>13</u>	Hepatoma-derived growth factor (HDGF)	17q2-q24	D17S794-D17S795
II	135.5		S75256 <u>14</u>	Neutrophil lipocalin (HNL)	-	-
II	110.4		X99133 <u>15</u>	Neutrophil gelatinase-associated lipocalin (NGAL)	9q34	D9S1821-D9S159
II	18.7		X85781 <u>16</u>	Nitric oxide synthase (NOS2)	[[?]]	-
II	15.1		X65965 <u>17</u>	Mitochondrial superoxide dismutase (SOD2)	6q25.3	D6S442-D6S1581
II	15.5	14.6	M22430 <u>18</u>	Phospholipase A2, group IIA (PLA2G2A)	1p35	-
II	15.3		X51441 <u>19</u>	Serum amyloid A (SAA)	11p	-
II	13.9		J03474 <u>20</u>	Serum amyloid A (SAA1)	11p15.1	D11S921-D11S1369
II	13.7		M21119 <u>21</u>	Lysozyme	-	-
II	13.4		D00408 <u>22</u>	Cytochrome P450 IIIA, polypeptide 7 (CPY3A7) (CYP3A7)	7	D7S479-D7S2545
II	14.2		D14662 <u>23</u>	Anti-oxidant protein 2	1	D1S2790-D1S2640
II	14.4		X64177 <u>24</u>	Metallothionein	-	-
II	18		J03910 <u>25</u>	Metallothionein-1G (MT1G)	16q13	D16S3057-D16S514
III	155	117.8	L08010 <u>26</u>	Regenerating islet-derived 1 β (REG1B)	2p12	D2S286-D2S169

III	†75	†36.4	J05412 <u>27</u>	Regenerating islet-derived 1 α (REG1A)	2p12	D2S139-D2S289
III	†9.7	†10.2	L15533 <u>28</u>	Panereatits Pancreatitis-associated protein (PAP)	2p12	D2S169-D2S139
III	†58.8		HC3566-HT3769 <u>29</u>	Zinc Finger Proteins	-	-
III	†55.1	†12.5	M87789 <u>30</u>	Ig γ 3 (IGHG3)	14q32.33	D14S65-qTEL
III	†17.5	†4.7	M26311 <u>31</u>	S100A9/calgranulin B	1q12-q22	D1S514-D1S2635
III	†10.8	†3.6	U08021 <u>32</u>	Nicotinamide N-methyltransferase (NNMT)	11q23.1	D11S1347-D11S939
III	†5		M72885 <u>33</u>	GOS2 <u>GOS2</u>	-	-
III	†3.9	†4.2	X65614 <u>34</u>	S100 calcium-binding protein (S100P)	4p16	-
III	†3.9		U01691 <u>35</u>	Annexin AV (ANXA5)	4q28-q32	D4S2945-D4S430
III	†3.7		U22431 <u>36</u>	Hypoxia-inducible factor 1 α (HIF1A)	14q21-q24	D14S1038-D14S290
III	†3.2		HC3494-HT3688 <u>37</u>	NF-116 <u>NF-IL6</u>	-	-
III		†3.3	X99585 <u>38</u>	Suppressor of mif two 3 (SMT3H2)	8	D8S257-D8S508
III		†3.1	U66617 <u>39</u>	SWI/SNF related regulator of chromatin (SMARCD1)	12q13-q14	D12S333-D12S325
III		†3.2	L19067 <u>40</u>	NF-kappa-B p65 subunit	-	-
III	†3.1	†3.2	D14520 <u>41</u>	Basic transcription element binding protein (2BTEB2)	-	-
III		†3.2	M21142 <u>42</u>	Guanine nucleotide-binding protein α (GNAS1)	20q13.2-q13.3	D20S183-D20S173
III		†4.9	AD000684 <u>43</u>	Liver specific bHLH-zip	-	-
III	†3.1		S37730 <u>44</u>	Insulin-like growth factor binding protein 2 (IGFBP2)	2q33-q34	D2S137-D2S164
III	†3.8		L11672 <u>45</u>	Zinc finger protein 91 (ZNF91)	19p13.1-p12	-
III	†3.8		D32257 <u>46</u>	Transcription factor IIIa	13q12.3-q13.1	D13S221-D13S1244
III	†5.5	†3.3	M32886 <u>47</u>	Sorcin (SRI)	7q21.1	D7S524-D7S657
III	†12.5	†5.9	M16364 <u>48</u>	Creatine kinase, brain (CKB)	14q32	D14S65-qTEL

IV	14.8		U21049 <u>49</u>	Epithelial Epithelial protein upregulated in carcinoma (DD96)	-	-
IV	13.5		D38583 <u>50</u>	Calgizzarin (S100A11)	7, 17, 4	D7S529-D7S4 84, D717s1352- D17S785
IV						D4S1615-D4S1579
IV		13.2	L42176 <u>51</u>	Downregulated in rhabdomyosarcoma (DRAL)	2q12-q14	D2S113-D2S176
IV	13.5		L07648 <u>52</u>	Max-interacting protein 1 (MXI1)	10q24-q25	D10S597-D10S1681
IV	14.4		L02785 <u>53</u>	Down regulated in adenoma (DRA)	7q31	D7S2420-D7S523
V	19.2		M57466 <u>54</u>	HLA-DPB1	6p21.3	D6S1558-D6S1616
V	15.9		HC3576- HT3779 <u>55</u>	MHC II β W52	-	-
V	15		HC1872- HT1907 <u>56</u>	MHC Dg	-	-
V	14.9		M33600 <u>57</u>	HLA-DRB1	6p21.3	D6S1558-D6S1616
V	14.1		X00274 <u>58</u>	HLA-DR α heavy chain	-	-
V	14		X62744 <u>59</u>	HLA-DMA	6p21.3	D6S1558-D6S1616
V	14		M16276 <u>60</u>	MHC II HLA-DR2-Dw12 DQw1- β	-	-
V	13.4		X03068 <u>61</u>	HLA-D II antigen DQw1.1 β	-	-
V	110.8		X57809 <u>62</u>	Ig λ gene cluster (IGL) <u>62</u>	22q11.1- q11.2	D22S420-D22S1144
V	19	13	L23566 <u>63</u>	Ig heavy chain, VDJRC	-	-
V	18.6		L02326 <u>64</u>	Ig λ -like polypeptide 2 (IGLL2)	22q11.2	D22S1144-D22S280
V	16.8		M63438 <u>65</u>	Ig rearranged γ chain, V- J-C region	-	-
V	15.6		X72475 <u>66</u>	Rearranged Ig κ light chain	-	-
V	14.6		M13560 <u>67</u>	Ia-associated invariant γ - chain (CD74)	-	-
V	14.1		M34516 <u>68</u>	Θ Ω light chain protein 14.1	-	-

V	14		X73079 <u>69</u>	Polymeric Ig receptor	-	-
V	13.7		S71043 <u>70</u>	Ig alpha 2 - IgA heavy chain allotype 2	-	-
V	13.7		X00437 <u>71</u>	T-cell specific protein/T-cell receptor	-	-
V	15.9		J03909 <u>72</u>	Interferon γ -inducible protein 30 (IFI30) (IP30)	19p13.1	D19S899-D19S407
V	13		M63838 <u>73</u>	Interferon γ -inducible protein (IFI16)	-	-
V		14.8	D28915 <u>74</u>	Microtubular aggregate protein p44	1	D1S203-D1S2865
V	14.2	13.4	M13755 <u>75</u>	Interferon stimulated protein 15-kDa (ISG15)	1	D1S243-D1S468
V		13.4	D11086 <u>76</u>	IL-2 receptor γ chain (IL2RG)	Xq13.1	DXS983-DXS995
V	13		M84526 <u>77</u>	Complement factor D (DF)	-	pTEL-D19S413
V	13.9		M38690 <u>78</u>	CD9 antigen	12p13	D12S99-D12S358
VI	120.4	140.8	M97925 <u>79</u>	Defensin 5 (DEFA5)	8pter-p21	D8S552-D8S549
VI	16.8	17.7	U33317 <u>80</u>	Defensin 6 (DEFA6)	8pter-p21	D8S277-D8S550
VII	116.2	13.3	L23808 <u>81</u>	MMP-12 (Macrophage elastase)	11q22.2-q22.3	D11S1339-D11S1343
VII	16.4		J05070 <u>82</u>	MMP-9 (Gelatinase B)	20q11.2-q13.1	D20S119-D20S197
VII	14.7		X54925 <u>83</u>	MMP-1 (Interstitial collagenase)	11q22.3	D11S1339-D11S1343
VII	14.2		X05232 <u>84</u>	MMP-3 (Stromelysin 1)	11q22.3	D11S1339-D11S1343
VII	113.3	13.8	L10343 <u>85</u>	Elastase specific inhibitor (Elafin)	20q12-q13	D20S119-D20S197
VII	111	13.1	Z74616 <u>86</u>	COL1A2	2q37	D2S2158-D2S125
VII	17.3		X52022 <u>87</u>	COL6A3	2q37	D2S2158-D2S125
VII	16.9	13.6	M55998 <u>88</u>	COL1A1	17q21.3-q22	D17S791-D17S794
VII	14.8		X06700 <u>89</u>	COL3A1	2q31	D2S2257-D2S115
VII	14.7		X15882 <u>90</u>	COL6A2	21q22.3	-
VII	13.9		X05610 <u>91</u>	COL4A2	13q34	D13S285-qTEL
VII	13.7	13.3	HG2157-HT2227 <u>92</u>	Mucin 4 (MUC4)	3q29	-

VII	13 .1		X52003 <u>93</u>	Trefoil factor 1 (TFF1)	21q22.3	D21S1259-qTEL
VII		14 .6	M22406 <u>94</u>	Intestinal mucin	-	-
VII	16 .4		J03040 <u>95</u>	Osteonectin (SPARC)	5q31.3-q32	D5S436-D5S470
VII	14	13 .2	X17042 <u>96</u>	Proteoglycan 1 (PRG1)	10q22.1	D10S210-D10S537
VII	13 .9		D11428 <u>97</u>	Peripheral myelin protein 22 (PMP22)	17p12-p11.2	D17S804-D17S799
VII	13 .8		X02761 <u>98</u>	Fibronectin 1 (FN1)	2q34	D2S137-D2S164
VII	13 .7		M77349 <u>99</u>	Transforming growth factor beta-induced (TGF β 1)	5q31	D5S393-D5S500
VII	13 .2		D13666 <u>100</u>	Osteoblast specific factor 2 (OSF-2)	13	D13S267-D13S1253
VII	13 .1		M10321 <u>101</u>	von Willebrand factor	12p13.3	D12S99-D12S358
VII	13		L09190 <u>102</u>	Trichohyalin (THH)	1q21-q23	D1S439-D1S459
VII		13 .1	D88422 <u>103</u>	Cystatin A (CSTA)	3q21	-
VII		14 .7	X58199 <u>104</u>	Adducin 2 (ADD2)	2p13-p14	-
VII		13 .7	M86933 <u>105</u>	Amelogenin (AMELY)	Yp11.2	-
VII		13 .2	D45370 <u>106</u>	Adipose specific collagen-like 2 (APM2)	10	D10S1786-D10S541
VII		13 .8	X73501 <u>107</u>	Cytokeratin 20	-	-
VIII	15 0.5		D28416 <u>108</u>	Esterase D (ESD)	13q14.1-q14.2	D13S328-D13S168
VIII	14 .7		M15656 <u>109</u>	Aldolase B	9q21.3-q22.2	D15S202-D15S157
VIII		16 .3	J04040 <u>110</u>	Glucagon (GCG)	2q36-q37	D2S156-D2S376
VIII		14 .4	L31801 <u>111</u>	Monocarboxylate transporter 1 (MCT1)	1p13.2-p12	D1S418-D1S514
VIII	13		D10523 <u>112</u>	Oxoglutarate dehydrogenase (OGDH)	7p14-p13	D7S521-D7S478
VIII	14		M12963 <u>113</u>	Alcohol dehydrogenase 1a (ADH1)	4q21-q23	-
VIII	14 .5		Y00339 <u>114</u>	Carbonic anhydrase II (CA2)	8q22	D8S275-D8S273
VIII	14 .9	13 .1	L10955 <u>115</u>	Carbonic anhydrase IV (CA4)	17q23	-

VIII	1 12.7	1 3.1	L05144 <u>116</u>	Phosphoenolpyruvate carboxykinase 1, soluble (PCK1)	20q13.31	D20S183-D20S173
VIII	1 3		U07158 <u>117</u>	Syntaxin 4A (STX4A)	-	-
VIII		1 3	L27706 <u>118</u>	Chaperonin subunit 6A (CCT6A)	7	D7S530-D7S509
VIII		1 3.1	J04093 <u>119</u>	UDP-glucosyltransferase UDP-glycosyltransferase 1 (UGT1)	2	D2S2158-D2S125
VIII	1 3.2		U20499 <u>120</u>	Sulfotransferase family 1A (SULT1A3)	16p11.2	-
VIII	1 3		M15182 <u>121</u>	β -glucuronidase (GUSB)	7q21.11	-
VIII	1 4		U08854 <u>122</u>	UDP glucuronosyltransferase precursor (UGT2B15)	4q13	D4S1619-D4S392
VIII	1 5		D87292 <u>123</u>	Thiosulfate sulfurtransferase (TST)	22	D22S277-D22S283
VIII	1 13	1 4	M22324 <u>124</u>	Aminopeptidase N/CD13 (ANPEP)	15q25-q26	D15S202-D15S157
VIII		1 7	M22960 <u>125</u>	Protective protein for b <u>beta</u> -galactosidase (PPGB)	20q13.1	D20S119-D20S197
VIII	1 3.4		X90908 <u>126</u>	Fatty acid binding protein 6 (FABP6)	5q23-q35	-
VIII		1 4.1	J02874 <u>127</u>	Fatty acid binding protein 4 (FABP4)	8q21	-
VIII	1 3		M10050 <u>128</u>	Fatty acid binding protein 1 (FABP1)	11p15.5	D11S1318-D11S909
VIII	1 3		L24774 <u>129</u>	Mitochondrial d3, d2-CoA-isomerase	-	-
VIII	1 4		D16294 <u>130</u>	Mitochondrial 3-oxoacyl-CoA thiolase (ACAA2)	18	D18S1118-D18S474
VIII	1 4		M77144 <u>131</u>	3 b <u>beta</u> -hydroxysteroid dehydrogenase (HSD3B2)[(D)]	1p13.1	D1S418-D1S514
VIII	1 5		D10511 <u>132</u>	Mitochondrial acetoacetyl-CoA thiolase	-	-
VIII	1 7		Z80345 <u>133</u>	Acyl-Coenzyme A dehydrogenase (ACADS)	12q22-qter	D12S366-D12S340
VIII	1 7		L11708 <u>134</u>	17 b <u>beta</u> -hydroxysteroid dehydrogenase II (HSD17B2)	16q24.1-q24.2	D16S515-D16S422

VIII	17		U26726 <u>135</u>	11 b beta-hydroxysteroid dehydrogenase II (HSD11B2)	16q22	D16S3031-D16S3139
VIII	13.5		X93036 <u>136</u>	MAT8 protein	19	D19S425-D19S418
VIII	12.2	14	M97496 <u>137</u>	Guanylate cyclase activator 1B 2A (UCA1B) (GUCA2A)	6p21.1	D1S2843-D1S417
VIII		14.2	D17400 <u>138</u>	6-pyruvoyl-tetrahydropterin synthase (PCBD) (PTPS)	10q22	D10S210-D10S537
VIII		13.3	D21262 <u>139</u>	KIAA0035	-	-
VIII		13.1	AB002365 <u>140</u>	KIAA0367	-	-
VIII		14.5	M11119 <u>141</u>	Endogenous retrovirus envelope region	-	-
VIII	13.1		M19961 <u>142</u>	Mitochondrial cytochrome c oxidase Vb (COX5B)	2cen-q13	D2S113-D2S176
VIII	13.1		D26129 <u>143</u>	Pancreatic ribonuclease (RNASE1)	14	pTEL-D14S283
VIII	13.1		U77643 <u>144</u>	K12 (SECTM1)	17q25	-
VIII	14		HC3991- HT4261 <u>145</u>	Cpg CpG-Enriched DNA, clone E18	=	=

V. Please insert the accompanying paper copy of the Sequence Listing, page numbers 1-132, at the end of the application.